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SEQUENCE LISTING

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<120> CAMP FACTOR OF STREPTOCOCCUS UBERIS

<130> 9000-0030.10

<140> 09/234,730

<141> 1999-01-21

<160> 5

<170> PatentIn Ver. 2.0

<210> 1

<211> 1191

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: *S. uberis* CAMP
factor gene

<220>

<221> CDS

<222> (157)..(924)

<400> 1

aatgaacata aaataaaaat taataattat atatttttat gataatcaca tatatttgac 60

ttaaaaaaat tggtactgta tgatacaggc ataagtactt atttatttta tagattgcaa 120

tttataaaca attatatattt tcaaagagga atgctt atg gaa ttc aaa aag tta 174
Met Glu Phe Lys Lys Leu
1 5

gtt tat tta act ggt tca atc gca gga att act tta ttt tcc cca att 222
Leu Tyr Leu Thr Gly Ser Ile Ala Gly Ile Thr Leu Phe Ser Pro Ile
10 15 20

tta aca aat gtc caa gca aat caa ata aat gtt aat caa caa tat aat
Ser Thr Ser Val Gln Ala Asn Gln Ile Asn Val Ser Gln Pro Ser Asn
25 30

aat gaa agt aat ggt att tca cag aac aaa gaa gaa att aat aat agt 27
Asn Glu Ser Asn Val Ile Ser Gln Lys Lys Glu Glu Ile Asp Asn Ser
35 40 45 50

cta aat cag gaa aat gct caa cta tat gcc ttc aaa gaa aat gtt aaa 300
Leu Asn Gln Gln Ser Ala Gln Ser Tyr Ala Ser Tyr Gln Asp Val Lys
55 60 65 70

aat tta aaa act tca ctt aga gct aat cct gaa aca att tat gat tta 462
 Asn Leu Lys Thr Ser Leu Arg Ala Asn Pro Glu Thr Ile Tyr Asp Leu
 90 95 100

aat tct att gga aca aga gta gaa gga atc cct gac gtg att caa gca 510
 Asn Ser Ile Gly Thr Arg Val Glu Ala Ile Ser Asp Val Ile Gln Ala
 105 110 115

att gtt ttt tca acg caa cag tta aca aat aaa gtt gat caa gct cag 558
 Ile Val Phe Ser Thr Gln Gln Leu Thr Asn Lys Val Asp Gln Ala His
 120 125 130

att gat atg gga ttt gct att acg aaa tta ctt att cgc att gca gac 606
 Ile Asp Met Gly Phe Ala Ile Thr Lys Leu Leu Ile Arg Ile Ala Asp
 135 140 145 150

cca ttt gct tca aat gaa tcc att aaa ggg caa gtc gaa gct gtt aaa 654
 Pro Phe Ala Ser Asn Glu Ser Ile Lys Gly Gln Val Glu Ala Val Lys
 155 160 165

caa gtg caa gag act gtg ctt acc tat ccc gat ttg cag cct acg gat 702
 Gln Val Gln Ala Thr Val Leu Thr Tyr Pro Asp Leu Gln Pro Thr Asp
 170 175 180

aga gca act att tac gtt aaa tca aaa tta gac aag ctt att tgg caa 750
 Arg Ala Thr Ile Tyr Val Lys Ser Lys Leu Asp Lys Leu Ile Trp Gln
 185 190 195

aca aga att acc aga gat caa aaa gtt ctt aat gta aag agt ttt gaa 798
 Thr Arg Ile Thr Arg Asp Gln Lys Val Leu Asn Val Lys Ser Phe Glu
 200 205 210

gtt tat cat caa tta aat aaa gct atc aca cat gca gta ggt gta caa 846
 Val Tyr His Gln Leu Asn Lys Ala Ile Thr His Ala Val Gly Val Gln
 215 220 225 230

tta aat cca act gta aca gtt gca caa gtt gac caa gaa atc aaa gtg 894
 Leu Asn Pro Thr Val Thr Val Ala Gln Val Asp Gln Glu Ile Lys Val
 235 240 245

cta caa gaa gca tta aat act gct cta cag taaggtagag attgaattga 944
 Leu Gln Glu Ala Leu Asn Thr Ala Leu Gln
 245 250

cttatcaaaa aactactgaaa tttatttatt tcaatccttt aaatatttta tttaactaat 1004

ttactttgttt aactadatttt ttgaaaaatt aattaccata cttcaatttt cttcaaatata 1004

cttgttatgtc catcccttc taaaacatag ctaattagtt tagttttctg gctaatadat 1124

tgtacatgaa attgtttcaaa attactaggg taaaagggttt ttcttttttat aaattcatea 1184

tgaactat 1191

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: CAMP factor
preprotein

<400> 1

Met Glu Phe Lys Lys Leu Leu Tyr Leu Thr Gly Ser Ile Ala Gly Ile
1 5 10 15

Thr Leu Phe Ser Pro Ile Leu Thr Ser Val Gln Ala Asn Gln Ile Asn
20 25 30

Val Ser Gln Pro Ser Asn Asn Glu Ser Asn Val Ile Ser Gln Lys Lys
35 40 45

Glu Glu Ile Asp Asn Ser Leu Asn Gln Glu Ser Ala Gln Leu Tyr Ala
50 55 60

Leu Lys Glu Asp Val Lys Gly Thr Glu Lys Glu Gln Ser Val Asn Ser
65 70 75 80

Ala Ile Ser Ala Val Glu Asn Leu Lys Thr Ser Leu Arg Ala Asn Pro
85 90 95

Glu Thr Ile Tyr Asp Leu Asn Ser Ile Gly Thr Arg Val Glu Ala Ile
100 105 110

Ser Asp Val Ile Gln Ala Ile Val Phe Ser Thr Gln Gln Leu Thr Asn
115 120 125

Lys Val Asp Gln Ala His Ile Asp Met Gly Phe Ala Ile Thr Lys Leu
130 135 140

Leu Ile Arg Ile Ala Asp Pro Phe Ala Ser Asn Glu Ser Ile Lys Gly
145 150 155 160

Gln Val Glu Ala Val Lys Gln Val Gln Ala Thr Val Leu Thr Tyr Pro
165 170 175

Asp Leu Gln Pro Thr Asp Arg Ala Thr Ile Tyr Val Lys Ser Lys Leu
180 185 190

Asp Lys Ile Ile Thr Gln Thr Asn Ile Thr Asn Asp Gln Tyr Val Leu
195 200 205

Asn Val Lys Ser Phe Glu Val Tyr His Gln Leu Asn Lys Ala Ile Thr
210 215 220

His Ala Val Gly Val Gln Leu Asn Pro Thr Val Thr Val Ala Gln Val
225 230 235 240

Asp Gln Glu Ile Lys Val Ser Gln Gln Ala Ser Asn Thr Ala Ser Gln
245 250 255

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: deduced *S. uberis*
CAMP factor protein

<400> 3

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Thr	Leu	Phe	Ser	Pro	Ile	Leu	Thr	Ser	Val	Gln	Ala	Asn	Gln	Ile	Asn	
			20				25						30			
Val	Ser	Gln	Pro	Ser	Asn	Asn	Glu	Ser	Asn	Val	Ile	Ser	Gln	Lys	Lys	
		35					40					45				
Glu	Glu	Ile	Asp	Asn	Ser	Leu	Asn	Gln	Glu	Ser	Ala	Gln	Leu	Tyr	Ala	
	50					55					60					
Leu	Lys	Glu	Asp	Val	Lys	Gly	Thr	Glu	Lys	Glu	Gln	Ser	Val	Asn	Ser	
65					70				75					80		
Ala	Ile	Ser	Ala	Val	Glu	Asn	Leu	Lys	Thr	Ser	Leu	Arg	Ala	Asn	Pro	
				85					90					95		
Glu	Thr	Ile	Tyr	Asp	Leu	Asn	Ser	Ile	Gly	Thr	Arg	Val	Glu	Ala	Ile	
		100							105				110			
Ser	Asp	Val	Ile	Gln	Ala	Ile	Val	Phe	Ser	Thr	Gln	Gln	Leu	Thr	Asn	
		115					120					125				
Lys	Val	Asp	Gln	Ala	His	Ile	Asp	Met	Gly	Phe	Ala	Ile	Thr	Lys	Leu	
	130					135					140					
Leu	Ile	Arg	Ile	Ala	Asp	Pro	Phe	Ala	Ser	Asn	Glu	Ser	Ile	Lys	Gly	
145				150						155				160		
Gln	Val	Glu	Ala	Val	Lys	Gln	Val	Gln	Ala	Thr	Val	Leu	Thr	Tyr	Pro	
			165					170						175		
Asp	Leu	Gln	Pro	Thr	Asp	Arg	Ala	Thr	Ile	Tyr	Val	Lys	Ser	Lys	Leu	
		180						185					190			
Asp	Lys	Leu	Ile	Trp	Gln	Thr	Arg	Ile	Thr	Arg	Asp	Gln	Lys	Val	Leu	
	195															
Asn	Val	Lys	Ser	Ala	Gln	Val	Tyr	His	Gln	Leu	Asn	Lys	Ala	Ile	Thr	
	210					215					220					
His	Ala	Val	Gly	Val	Gln	Leu	Asn	Pro	Thr	Val	Thr	Val	Ala	Gln	Val	
225					230					235				240		
Asp	Gln	Gln	Ile	Lys	Val	Leu	Gln	Gln	Ala	Leu	Asn	Thr	Ala	Leu	Gln	

<210> 4
<211> 226
<212> PRT
<213> Artificial Sequence

<220>
<221> Description of Artificial Sequence: *S. agalactiae*
CAMP factor protein

<400> 4
Asp Gln Val Thr Thr Pro Gln Val Val Asn His Val Asn Ser Asn Asn
1 5 10 15
Gln Ala Gln Gln Met Ala Gln Lys Leu Asp Gln Asp Ser Ile Gln Leu
20 25 30
Arg Asn Ile Lys Asp Asn Val Gln Gly Thr Asp Tyr Glu Lys Pro Val
35 40 45
Asn Glu Ala Ile Thr Ser Val Glu Lys Leu Lys Thr Ser Leu Arg Ala
50 55 60
Asn Ser Glu Thr Val Tyr Asp Leu Asn Ser Ile Gly Ser Arg Val Glu
65 70 75 80
Ala Leu Thr Asp Val Ile Glu Ala Ile Thr Phe Ser Thr Gln His Leu
85 90 95
Ala Asn Lys Val Ser Gln Ala Asn Ile Asp Met Gly Phe Gly Ile Thr
100 105 110
Lys Leu Val Ile Arg Ile Leu Asp Pro Phe Ala Ser Val Asp Ser Ile
115 120 125
Lys Ala Gln Val Asn Asp Val Lys Ala Leu Glu Gln Lys Val Leu Thr
130 135 140
Tyr Pro Asp Leu Lys Pro Thr Asp Arg Ala Thr Ile Tyr Thr Lys Ser
145 150 155 160
Lys Leu Asp Lys Glu Ile Trp Asn Thr Arg Phe Thr Arg Asp Lys Lys
165 170 175
Val Leu Asn Val Lys Gln Phe Lys Val Tyr Asn Thr Leu Asn Lys Ala
180 185 190
Ile Gln His Ala Val Gly Val Gln Leu Asn Pro Asn Val Thr Val Gln
195 200 205
Gln Val Asp Gln Gln Ile Val Thr Leu Gln Ala Ala Leu Gln Thr Ala
210 215 220
Leu Lys

<211> 228

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: mature *S. uberis*
CAMP factor protein

<400> 5

Asn Gln Ile Asn Val Ser Gln Pro Ser Asn Asn Glu Ser Asn Val Ile
1 5 10 15

Ser Gln Lys Lys Glu Gln Ile Asp Asn Ser Leu Asn Gln Glu Ser Ala
20 25 30

Gln Leu Tyr Ala Leu Lys Glu Asp Val Lys Gly Thr Glu Lys Glu Gln
35 40 45

Ser Val Asn Ser Ala Ile Ser Ala Val Glu Asn Leu Lys Thr Ser Leu
50 55 60

Arg Ala Asn Pro Glu Thr Ile Tyr Asp Leu Asn Ser Ile Gly Thr Arg
65 70 75 80

Val Glu Ala Ile Ser Asp Val Ile Gln Ala Ile Val Phe Ser Thr Gln
85 90 95

Gln Leu Thr Asn Lys Val Asp Gln Ala His Ile Asp Met Gly Phe Ala
100 105 110

Ile Thr Lys Leu Leu Ile Arg Ile Ala Asp Pro Phe Ala Ser Asn Glu
115 120 125

Ser Ile Lys Gly Gln Val Glu Ala Val Lys Gln Val Gln Ala Thr Val
130 135 140

Leu Thr Tyr Pro Asp Leu Gln Pro Thr Asp Arg Ala Thr Ile Tyr Val
145 150 155 160

Lys Ser Lys Leu Asp Lys Leu Ile Trp Gln Thr Arg Ile Thr Arg Asp
165 170 175

Gln Lys Val Leu Asn Val Lys Ser Phe Gln Val Tyr His Gln Leu Asn
180 185 190

Lys Ala Ile Thr Ile Ala Val Gly Val Gln Leu Asn Pro Thr Val Thr
195 200 205

Val Ala Gln Val Asp Gln Gln Ile Lys Val Leu Gln Gln Ala Leu Asn
210 215 220

Thr Ala Leu Gln
225